PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/712,302*

1812

DATE: 02/03/98
TIME: 20:36:40

INPUT SET: S23147.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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1                              SEQUENCE LISTING
2
3   (1)    General Information:
4
5        (i) APPLICANT: Grotendorst, Gary R.
6                       Bradham Jr., Douglas M.,
7
8       (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
9
10     (iii) NUMBER OF SEQUENCES: 2
11
12      (iv) CORRESPONDENCE ADDRESS:
13            (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
14            (B) STREET: 4225 Executive Square, Suite 1400
15            (C) CITY: La Jolla
16            (D) STATE: CA
17            (E) COUNTRY: US
18            (F) ZIP: 92037
19
20       (v) COMPUTER READABLE FORM:
21            (A) MEDIUM TYPE: Floppy disk
22            (B) COMPUTER: IBM PC compatible
23            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26      (vi) CURRENT APPLICATION DATA:
27            (A) APPLICATION NUMBER: 08/712,302
28            (B) FILING DATE: 11-SEP-1996
29            (C) CLASSIFICATION: 435
30
31     (vii) PRIOR APPLICATION DATA:
32            (A) APPLICATION NUMBER: US 08/386,680
33            (B) FILING DATE: 10-FEB-1995
34
35            (A) APPLICATION NUMBER: US/08/167,628
36            (B) FILING DATE:
37
38            (A) APPLICATION NUMBER: US/07/752,427
39            (B) FILING DATE:
40
41    (viii) ATTORNEY/AGENT INFORMATION:
42            (A) NAME: Wetherell, Jr. Ph.D., John W.
43            (B) REGISTRATION NUMBER: 31,678
44            (C) REFERENCE/DOCKET NUMBER: PD-1294
45
46      (ix) TELECOMMUNICATION INFORMATION:
```

```
47          (A) TELEPHONE: 619-455-5100
48          (B) TELEFAX: 619-455-5110
49
50
51   (2) INFORMATION FOR SEQ ID NO:1:
52
53      (i) SEQUENCE CHARACTERISTICS:
54          (A) LENGTH: 2075 base pairs
55          (B) TYPE: nucleic acid
56          (C) STRANDEDNESS: single
57          (D) TOPOLOGY: linear
58
59     (ii) MOLECULE TYPE: cDNA
60
61
62    (vii) IMMEDIATE SOURCE:
63          (B) CLONE: DB60R32
64
65     (ix) FEATURE:
66          (A) NAME/KEY: CDS
67          (B) LOCATION: 130..1177
68
69
70     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
71
72   CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG          60
73
74   CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA         120
75
76   GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC             168
77            Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe
78             1               5                  10
79
80   GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC          216
81   Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys
82       15                  20                  25
83
84   AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG          264
85   Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala
86    30                  35                  40                  45
87
88   GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC          312
89   Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala
90               50                  55                  60
91
92   AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC          360
93   Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His
94               65                  70                  75
95
96   AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC          408
97   Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly
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99
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PATENT APPLICATION *US/08/712,302*

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101   Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val
102        95                  100                 105
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104   TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG   504
105   Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr
106   110                 115                 120                 125
107
108   TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT   552
109   Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val
110                 130                 135                 140
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112   CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC   600
113   Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro
114                 145                 150                 155
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116   GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC   648
117   Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr
118        160                 165                 170
119
120   GTG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC   696
121   Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly
122        175                 180                 185
123
124   CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG   744
125   Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu
126   190                 195                 200                 205
127
128   TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT   792
129   Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val
130                 210                 215                 220
131
132   ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC   840
133   Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys
134                 225                 230                 235
135
136   ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC   888
137   Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly
138        240                 245                 250
139
140   AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG   936
141   Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu
142        255                 260                 265
143
144   CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA   984
145   Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly
146   270                 275                 280                 285
147
148   GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG   1032
149   Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu
150                 290                 295                 300
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152   CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG   1080
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INPUT SET: S23147.raw

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154                 305             310             315
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156     ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT         1128
157     Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn
158                 320             325             330
159
160     GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T        1177
161     Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
162                 335             340             345
163
164     GAAGCCAGAG AGTGAGAGAC ATTAACTCAT TAGACTGGAA CTTGAACTGA TTCACATCTC        1237
165
166     ATTTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG        1297
167
168     GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC        1357
169
170     CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGA ACTACATTAG TACACAGCAC        1417
171
172     CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT        1477
173
174     CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA        1537
175
176     AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC        1597
177
178     CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA        1657
179
180     CATTCTGATT CGAATGACAC TGTTCAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT        1717
181
182     TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAAATATT        1777
183
184     GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA        1837
185
186     AGTTGTTTGT GCCTTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA        1897
187
188     TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT        1957
189
190     ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA        2017
191
192     GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG          2075
193
194
195     (2) INFORMATION FOR SEQ ID NO:2:
196
197             (i) SEQUENCE CHARACTERISTICS:
198                 (A) LENGTH: 349 amino acids
199                 (B) TYPE: amino acid
200                 (D) TOPOLOGY: linear
201
202             (ii) MOLECULE TYPE: protein
203
204             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
205
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INPUT SET: S23147.raw

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206  Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
207   1               5               10                  15

209  Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
210              20               25               30

212  Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
213          35               40               45

215  Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
216      50               55               60

218  Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
219   65               70               75               80

221  Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
222              85               90                   95

224  Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
225              100              105              110

227  Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
228          115              120              125

230  Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
231      130              135              140

233  Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
234  145              150              155              160

236  Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
237              165              170              175

239  Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
240          180              185              190

242  Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
243          195              200              205

245  Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
246      210              215              220

248  Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
249  225              230              235              240

251  Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
252              245              250              255

254  Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
255          260              265              270

257  Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
258      275              280              285
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/712,302*

INPUT SET: S23147.raw

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